

Project Report: Whole genome comparisons and the Evolution of Methane and Sulfur Metabolisms

Project Investigator:

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Project Progress

Sorel Fitz-Gibbon collaborated with Todd Lowe (University of California Santa Cruz) on functional analysis of the hyperthermophilic crenarchaeon *Pyrobaculum aerophilum* using full-genome DNA microarrays. The analysis suggests that a set of key sulfur metabolism genes found in this organism function in the reductive direction, reducing sulfate, rather than the proposed alternative, sulfur species oxidation. Additionally, the demonstrated regulation of these genes in response to oxygen suggests that frameshift disruptions found for one key enzyme are due to recent events. This together with the report of a sulfate reduction phenotype in the crenarchaeon *Caldivirga maquilgensis* (Itoh et al, 1999) suggests that sulfate reduction may be far more common among the Crenarchaeota than previously assumed.

Sorel Fitz-Gibbon and Christopher House Pennsylvania State University (PSU) continued their collaboration using whole genome sequences to study phylogenetic relationships. Initial steps have been taken to include incomplete genome sequences into their analyses. This will allow perhaps hundreds of additional organisms to be represented, significantly increasing the diversity and depth of resolution of the resulting trees.

Highlights

- Regulation in response to oxygen of *Pyrobaculum aerophilum*'s divergent sulfate reduction genes leads to the suggestion that sulfate reduction may be far more common among the Crenarchaeota (and, more generally, the Archaea) than previously assumed.

Roadmap Objectives

- **Objective No. 4.1:** Earth's early biosphere
- **Objective No. 4.2:** Foundations of complex life
- **Objective No. 6.1:** Environmental changes and the cycling of elements by the biota, communities, and ecosystems